CRF Errors Corrected by the STIC Systems Branch

ENTERED

Serial Number: 09/826,115

CRF Processing Date: 4/18/2001
Edited by: _____
Verified by: _____ AN (STIC staff)

- [ ] Changed a file from non-ASCII to ASCII.

- [ ] Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- [ ] Edited a format error in the Current Application Data section, specifically: _____

- [ ] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was [ ] the prior application data; or [ ] other _____

- [ ] Added the mandatory heading and subheadings for "Current Application Data".

- [ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- [ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

- [ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

- [ ] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

- [ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- [ ] Inserted colons after headings/subheadings. Headings edited included: _____

- [ ] Deleted extra, invalid, headings used by an applicant, specifically: _____

- [ ] Deleted: [ ] non-ASCII "garbage" at the beginning/end of files; [ ] secretary initials/filename at end of file; [ ] page numbers throughout text; [ ] other invalid text, such as _____

- [ ] Inserted mandatory headings, specifically: _____

- [ ] Corrected an obvious error in the response, specifically: _____

- [ ] Edited identifiers where upper case is used but lower case is required, or vice versa.

- [ ] Corrected an error in the Number of Sequences field, specifically: _____

- [ ] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted

- [ ] Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- [x] Other: Sequence 7 - corrected (2227 responses) _____

_____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

```
          RAW SEQUENCE LISTING              DATE: 04/18/2001
          PATENT APPLICATION:  US/09/826,115    TIME: 16:42:46

          Input Set : A:\PTO.txt
          Output Set: N:\CRF3\04182001\I826115.raw
```

```
     4 <110> APPLICANT: Chang, Gwong-Jen J
     6 <120> TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
     7        Flavivirus Infection
     9 <130> FILE REFERENCE: 14114.0332U3
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/826,115
C--> 11 <141> CURRENT FILING DATE: 2001-04-04
    11 <150> PRIOR APPLICATION NUMBER: pct/us99/12298
    12 <151> PRIOR FILING DATE: 1999-06-03
    14 <150> PRIOR APPLICATION NUMBER: 09/701,536
    15 <151> PRIOR FILING DATE: 2000-11-29
    17 <150> PRIOR APPLICATION NUMBER: 60/087,908
    18 <151> PRIOR FILING DATE: 1998-06-04
    20 <160> NUMBER OF SEQ ID NOS: 31
    22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
    24 <210> SEQ ID NO: 1
    25 <211> LENGTH: 48
    26 <212> TYPE: DNA
    27 <213> ORGANISM: Artificial Sequence
    29 <220> FEATURE:
    30 <223> OTHER INFORMATION: Description of artificial sequence; note =
    31        synthetic construct
    33 <221> NAME/KEY: CDS
    34 <222> LOCATION: (25)...(48)
    36 <221> NAME/KEY: misc_feature
    37 <222> LOCATION: 1-48
    38 <223> OTHER INFORMATION: Amplimer 14DV389
    40 <400> SEQUENCE: 1
    41 cttggtacct ctagagccgc cgcc atg ggc aga aag caa aac aaa aga        48
    42                          Met Gly Arg Lys Gln Asn Lys Arg
    43                          1               5
    46 <210> SEQ ID NO: 2
    47 <211> LENGTH: 8
    48 <212> TYPE: PRT
    49 <213> ORGANISM: Artificial Sequence
    51 <220> FEATURE:
    52 <223> OTHER INFORMATION: Description of artificial sequence; note =
    53        synthetic construct
    55 <400> SEQUENCE: 2
    56 Met Gly Arg Lys Gln Asn Lys Arg
    57 1               5
    59 <210> SEQ ID NO: 3
    60 <211> LENGTH: 50
    61 <212> TYPE: DNA
    62 <213> ORGANISM: Artificial Sequence
    64 <220> FEATURE:
    65 <223> OTHER INFORMATION: Description of artificial sequence; note =
    66        synthetic construct
```

RAW SEQUENCE LISTING   DATE: 04/18/2001
PATENT APPLICATION: US/09/826,115   TIME: 16:42:46

Input Set : A:\PTO.txt
Output Set: N:\CRF3\04182001\I826115.raw

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68 <221> NAME/KEY: misc_feature
69 <222> LOCATION: 1-50
70 <223> OTHER INFORMATION: Amplimer c14DV2453
72 <400> SEQUENCE: 3
73 ttttcttttg cggccgctca aacttaagca tgcacattgg tcgctaagaa          50
75 <210> SEQ ID NO: 4
76 <211> LENGTH: 48
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Description of artificial sequence; note =
82       synthetic construct
84 <221> NAME/KEY: CDS
85 <222> LOCATION: (25)...(48)
87 <221> NAME/KEY: misc_feature
88 <222> LOCATION: (1)...(48)
89 <223> OTHER INFORMATION: Amplimer YFDV389
91 <400> SEQUENCE: 4
92 cttggtacct ctagagccgc cgcc atg cgt tcc cat gat gtt ctg act       48
93                            Met Arg Ser His Asp Val Leu Thr
94                            1               5
97 <210> SEQ ID NO: 5
98 <211> LENGTH: 8
99 <212> TYPE: PRT
100 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Description of artificial sequence; note =
104       synthetic construct
106 <400> SEQUENCE: 5
107 Met Arg Ser His Asp Val Leu Thr
108 1               5
110 <210> SEQ ID NO: 6
111 <211> LENGTH: 41
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Description of artificial sequence; note =
117       synthetic construct
119 <221> NAME/KEY: misc_feature
120 <222> LOCATION: 1-41
121 <223> OTHER INFORMATION: Amplimer cYFDV2452
123 <400> SEQUENCE: 6
124 ttttcttttg cggccgctca cgccccaact cctagagaaa c                    41
126 <210> SEQ ID NO: 7
127 <211> LENGTH: 51
128 <212> TYPE: DNA
129 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION: Description of artificial sequence; note =
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    133       synthetic construct
    135 <221> NAME/KEY: CDS              1
W--> 136 <222> LOCATION: (25)...(54)
    138 <221> NAME/KEY: misc_feature
W--> 139 <222> LOCATION: 1-54  51
    140 <223> OTHER INFORMATION: Amplimer SLEDV410
    142 <400> SEQUENCE: 7
    143 cttggtacct ctagagccgc cgcc atg tct aaa aaa aga gga ggg acc aga        51
    144                           Met Ser Lys Lys Arg Gly Gly Thr Arg
    145                            1                 5
    148 <210> SEQ ID NO: 8
    149 <211> LENGTH: 9
    150 <212> TYPE: PRT
    151 <213> ORGANISM: Artificial Sequence
    153 <220> FEATURE:
    154 <223> OTHER INFORMATION: Description of artificial sequence; note =
    155       synthetic construct
    157 <400> SEQUENCE: 8
    158 Met Ser Lys Lys Arg Gly Gly Thr Arg
    159  1                 5
    161 <210> SEQ ID NO: 9
    162 <211> LENGTH: 38
    163 <212> TYPE: DNA
    164 <213> ORGANISM: Artificial Sequence
    166 <220> FEATURE:
    167 <223> OTHER INFORMATION: Description of artificial sequence; note =
    168       synthetic construct
    170 <221> NAME/KEY: misc_feature
    171 <222> LOCATION: 1-38
    172 <223> OTHER INFORMATION: Amplimer cSLEDV2449
    174 <400> SEQUENCE: 9
    175 ttttcttttg cggccgctta ggcttgcacg ctggttgc                             38
    177 <210> SEQ ID NO: 10
    178 <211> LENGTH: 7500
    179 <212> TYPE: DNA
    180 <213> ORGANISM: Artificial Sequence
    182 <220> FEATURE:
    183 <223> OTHER INFORMATION: Description of artificial sequence; note =
    184       synthetic construct
    186 <221> NAME/KEY: CDS
    187 <222> LOCATION: (916)...(3009)
    189 <221> NAME/KEY: misc_feature
    190 <222> LOCATION: 1-7500
    191 <223> OTHER INFORMATION: pCDJE 2-7
    193 <400> SEQUENCE: 10
    194 gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg      60
    195 ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg     120
    196 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc     180
    197 ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt     240
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198 gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata      300
199 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360
200 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
201 attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt      480
202 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
203 atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca      600
204 tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660
205 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc      720
206 aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg      780
207 gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca      840
208 ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc      900
209 gagctcgccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa      951
210              Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
211                1                5                    10
213 ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg      999
214 Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
215        15                20                25
217 gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc     1047
218 Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
219     30                35                40
221 aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga     1095
222 Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
223 45                50                55                    60
225 gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag     1143
226 Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
227                65                70                75
229 gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca     1191
230 Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
231            80                85                90
233 gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat     1239
234 Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr
235        95                100                105
237 gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg     1287
238 Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val
239     110                115                120
241 tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct     1335
242 Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala
243 125                130                135                    140
245 tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac     1383
246 Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn
247                145                150                155
249 tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc     1431
250 Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly
251                160                165                170
253 tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc     1479
254 Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu
255        175                180                185
257 ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc     1527
258 Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly
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259     190                   195                  200
261 aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg    1575
262 Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu
263 205                   210                  215                 220
265 gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca    1623
266 Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro
267                   225                  230                 235
269 aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag    1671
270 Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu
271                   240                  245                 250
273 gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg    1719
274 Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val
275             255                  260                  265
277 gct cgg tgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat    1767
278 Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp
279     270                   275                  280
281 agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac    1815
282 Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn
283 285                   290                  295                 300
285 gga tgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc    1863
286 Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe
287             305                  310                  315
289 tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc    1911
290 Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile
291             320                  325                  330
293 aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac    1959
294 Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn
295             335                  340                  345
297 cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt    2007
298 His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe
299     350                   355                  360
301 aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac    2055
302 Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr
303 365                   370                  375                 380
305 gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa    2103
306 Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu
307             385                  390                  395
309 gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg    2151
310 Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg
311             400                  405                  410
313 gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca    2199
314 Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr
315             415                  420                  425
317 gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc    2247
318 Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala
319     430                   435                  440
321 aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat    2295
322 Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His
323 445                   450                  455                 460
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/826,115

DATE: 04/18/2001
TIME: 16:42:47

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\04182001\I826115.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:136 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:7, CDS LOCATION: (25)...
(54)